

# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/593,213  
Source: IFwp  
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IFWP

**RAW SEQUENCE LISTING**  
 PATENT APPLICATION: US/10/593,213

DATE: 09/28/2006  
 TIME: 11:12:35

Input Set : A:\2107-299.ST25.txt  
 Output Set: N:\CRF4\09282006\J593213.raw

3 <110> APPLICANT: Lotz, Henrike  
 4       Brunner, Herwig  
 5       Rupp, Steffen  
 7 <120> TITLE OF INVENTION: Hyphae-Specific Cell Wall Proteins of Candida (As Amended)  
 9 <130> FILE REFERENCE: P/2107-299  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/593,213  
 C--> 12 <141> CURRENT FILING DATE: 2006-09-15  
 14 <150> PRIOR APPLICATION NUMBER: 10 2004 013 826.5  
 15 <151> PRIOR FILING DATE: 2004-03-16  
 17 <160> NUMBER OF SEQ ID NOS: 15  
 19 <170> SOFTWARE: PatentIn version 3.3  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 336  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Candida Albicans  
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 29 gattcatcag ctgctgcctc tggtgctgcc tcggctgctt ctgggtccaa atctgggtct   120  
 31 acctcagctg cttctgtgc caaatccggt gcttcttcag ttgcttctgc cgctaaatct   180  
 33 ggtgtttctt cagctgcctc agctgctaaa tctggtgctt catctgctac cggtgggtca   240  
 35 tctgctgcca aatctggctc atcaagtggc gccgggtttg ctccctgtcgc tggtgctgg   300  
 37 agcttggcag ccattgctgg tcttttgg tttgtaa                                   336  
 40 <210> SEQ ID NO: 2  
 41 <211> LENGTH: 111  
 42 <212> TYPE: PRT  
 43 <213> ORGANISM: Candida Albicans  
 45 <400> SEQUENCE: 2  
 47 Met Lys Phe Ser Thr Thr Leu Leu Ala Leu Thr Ala Ser Ile Ala Ala  
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 52       20           25               30  
 55 Ala Ser Gly Ala Lys Ser Gly Ala Thr Ser Ala Ala Ser Gly Ala Lys  
 56       35           40               45  
 59 Ser Gly Ala Ser Ser Val Ala Ser Ala Ala Lys Ser Gly Val Ser Ser  
 60       50           55               60  
 63 Ala Ala Ser Ala Ala Lys Ser Gly Ala Ser Ser Ala Thr Gly Gly Ser  
 64       65           70               75               80  
 67 Ser Ala Ala Lys Ser Gly Ser Ser Ser Gly Ala Gly Phe Ala Pro Val  
 68       85           90               95  
 71 Ala Gly Ala Gly Ser Leu Ala Ala Ile Ala Gly Leu Leu Leu Leu  
 72       100           105             110  
 75 <210> SEQ ID NO: 3  
 76 <211> LENGTH: 507

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77 <212> TYPE: DNA  
 78 <213> ORGANISM: Candida Albicans  
 80 <400> SEQUENCE: 3  
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 85 aagaccgatt atattaaatt tttgccacc gaaaaagatg ttccaggtga tttatctacg 180  
 87 ttggctacca aagtgttgc ttatactgat gattcataca caacttggtaaatgatgat 240  
 89 tcttgaatg tttccaaactt agaagcatat gctactagtt tgccatggta ttccagaatt 300  
 91 caagctgatg ctggcggcaa aggttctgcc tccggctc cctctggctc tggttctgcc 360  
 93 aaatcaactg caagtgtga aaaaatctagt ggctcaagtg cttctgctc aagcaactgca 420  
 95 ggtggttcct cttctaaagg tgggtgaagt gaacttggtaatcctgttgg tgctgttgg 480  
 97 ggtgcttgg cagttgtttt aatgtaa 507  
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 101 <211> LENGTH: 168  
 102 <212> TYPE: PRT  
 103 <213> ORGANISM: Candida Albicans  
 105 <400> SEQUENCE: 4  
 107 Met Arg Phe Ala Phe Thr Thr Val Ser Leu Ser Leu Leu Leu Ser Ser  
 108 1 5 10 15  
 111 Leu Val Ala Ser Glu Ala Ala Ser Ser Asp Val Gln Phe Leu Thr Ala  
 112 20 25 30  
 115 Leu Val Gly Asp Tyr Gln Asp His Lys Thr Asp Tyr Ile Lys Phe Phe  
 116 35 40 45  
 119 Ala Thr Ala Lys Asp Val Pro Gly Asp Leu Ser Thr Leu Ala Thr Lys  
 120 50 55 60  
 123 Val Leu Thr Tyr Thr Asp Asp Ser Tyr Thr Thr Leu Leu Asn Asp Asp  
 124 65 70 75 80  
 127 Ser Leu Asn Val Ser Asn Leu Glu Ala Tyr Ala Thr Ser Leu Pro Trp  
 128 85 90 95  
 131 Tyr Ser Arg Ile Gln Ala Asp Ala Gly Gly Lys Gly Ser Ala Ser Gly  
 132 100 105 110  
 135 Ser Ala Ser Gly Ser Gly Ser Ala Lys Ser Thr Ala Ser Ala Glu Lys  
 136 115 120 125  
 139 Ser Ser Gly Ser Ser Ala Ser Ala Ser Ser Thr Ala Gly Gly Ser Ser  
 140 130 135 140  
 143 Ser Lys Gly Gly Val Ser Glu Leu Val Ala Pro Val Gly Ala Val Val  
 144 145 150 155 160  
 147 Gly Ala Leu Ala Val Ala Leu Met  
 148 165  
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 152 <211> LENGTH: 1682  
 153 <212> TYPE: DNA  
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 157 atgataatct ttcggaaatc tttttcact ttttggctt tgcttaattc tgtcttagct 60  
 159 cttgttatca ctcaaaacag agtcgatgt ggtgttctt acgttagtgt tgaaaatatc 120  
 161 accatcaatt ctggagcttc ttggtaatt atcaacaatg ctatataaac ccttggtaa 180  
 163 agtttaactg ttcagccaa tgctggctt tacattaccc tgacttcacc cctttgtca 240  
 165 cttcaagtca cattaacttc tttgcttagc acaattcaaa acaatggat tattgcgttc 300

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167	aattccctgc	cttccttaac	atcgccaca	tataatttag	ttggtttatac	ccttgtcaac	360										
169	actggagaaa	tgtattttc	tgcttctgg	gtttcaccta	gtgttatggc	tcttactgct	420										
171	gcatcttgg	caaacagtgg	attgatggca	tttatcaaa	atcaaagaag	ttctggatt	480										
173	gttagtctt	ggacaccatc	aggccaata	accaataatg	gtcaaatctg	tttgattaac	540										
175	gaagtctaca	aacagaccac	aagcatcaac	ggttctgg	gtttcaactgc	caatcgtaac	600										
177	tcgacaatat	atattgccaa	tgtattgtt	ccagttcca	catcgaaaa	tttttattt	660										
179	gcagacagcc	aatctccat	aattgttcaa	gctatttcaa	ccctcaagt	gtttaatgtc	720										
181	tatgggttt	gtaacggtaa	tatggtcgg	gttactctt	cattgatcg	taatatatgg	780										
183	aatccagcat	atagttataa	tccatccaca	ggtatttaa	gattgagaaa	ttttttgtg	840										
185	tatcaagatt	ttaatattgg	tcctgg	tatcttagt	tatttctgat	cgttactgac	900										
187	aatggtgctg	gtcttccctc	aacaataactc	ggttcggtt	cttatagtgg	tcctgttcca	960										
189	ccaagagctt	tacccgcac	ttgtaagatt	gcatgtaaac	ccgtgcctac	cgcgcagg	1020										
191	actaatccaa	ccgagtagac	gaccacaata	acaacaacaa	attctgtgg	taagccattg	1080										
193	acagaaactg	gtgtgg	tattctgact	gatagtaacg	gatcatgtt	ctcaagtact	1140										
195	acaatcttc	caactcg	gtcaagt	agcagtagca	gcactgtt	ttcaactgct	1200										
197	ccgtcatc	caagcac	accttcatc	agtagccaa	catcttctac	tccaccacca	1260										
199	tcttcaagta	gtaaagcatc	atcaactact	ccaagctct	gtagtcaatc	gtcttcaact	1320										
201	actccaagct	caagcagtaa	gccttcc	actgtaccac	caactggcag	cagtcaagtca	1380										
203	tcttcaacta	tcccaagttc	cagtaactaa	ccttcttct	ctgctccatc	atcttaagt	1440										
205	tctccatctt	cttctactac	tccaagctt	agcagtcaat	cttcattt	tgctcaaagc	1500										
207	tctattggcc	agacatcg	ttctactgt	tcttcgtc	gtagtcaacc	atctgtctgg	1560										
209	gagtcatcaa	gcagtcagtc	gtcatccgg	acgacaagtt	ccagtagtca	gttttcttca	1620										
211	agtccccac	cgtcaagtac	acaatctct	tttactgct	aaagctccaa	tagtcaatta	1680										
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217	<211>	LENGTH:	560														
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219	<213>	ORGANISM:	Candida Albicans														
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227	Ser	Val	Leu	Ala	Leu	Val	Ile	Thr	Gln	Asn	Arg	Val	Asp	Arg	Gly	Val	
228					20			25			30						
231	Leu	Asp	Val	Ser	Val	Gly	Asn	Ile	Thr	Ile	Asn	Ser	Gly	Ala	Ser	Trp	
232					35			40			45						
235	Ser	Ile	Ile	Asn	Asn	Ala	Ile	Ser	Thr	Leu	Val	Gly	Ser	Leu	Thr	Val	
236					50			55			60						
239	Gln	Pro	Asn	Ala	Gly	Leu	Tyr	Ile	Thr	Ser	Thr	Ser	Pro	Leu	Leu	Ser	
240					65			70			75			80			
243	Leu	Gln	Val	Thr	Leu	Thr	Ser	Leu	Leu	Ser	Thr	Ile	Gln	Asn	Asn	Gly	
244					85			90			95						
247	Ile	Ile	Ala	Phe	Asn	Ser	Ser	Pro	Ser	Leu	Thr	Ser	Ser	Thr	Tyr	Asn	
248					100			105			110						
251	Leu	Val	Gly	Leu	Ser	Leu	Val	Asn	Thr	Gly	Glu	Met	Tyr	Phe	Ser	Ala	
252					115			120			125						
255	Ser	Gly	Val	Leu	Pro	Ser	Val	Met	Ala	Leu	Thr	Ala	Ala	Ser	Trp	Ser	
256					130			135			140						
259	Asn	Ser	Gly	Leu	Met	Ala	Phe	Tyr	Gln	Asn	Gln	Arg	Ser	Ser	Gly	Ile	
260					145			150			155			160			

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263 Val Ser Leu Gly Thr Pro Ser Gly Ser Ile Thr Asn Asn Gly Gln Ile  
264 165 170 175  
267 Cys Leu Ile Asn Glu Val Tyr Lys Gln Thr Thr Ser Ile Asn Gly Ser  
268 180 185 190  
271 Gly Cys Phe Thr Ala Asn Arg Asn Ser Thr Ile Tyr Ile Ala Asn Val  
272 195 200 205  
275 Leu Leu Pro Val Ser Thr Ser Gln Asn Phe Tyr Leu Ala Asp Ser Gln  
276 210 215 220  
279 Ser Ser Ile Ile Val Gln Ala Ile Ser Thr Pro Gln Val Phe Asn Val  
280 225 230 235 240  
283 Tyr Gly Phe Gly Asn Gly Asn Met Val Gly Val Thr Leu Pro Leu Ile  
284 245 250 255  
287 Gly Asn Ile Trp Asn Pro Ala Tyr Ser Tyr Asn Pro Ser Thr Gly Ile  
288 260 265 270  
291 Leu Arg Leu Arg Asn Phe Phe Val Tyr Gln Asp Phe Asn Ile Gly Pro  
292 275 280 285  
295 Gly Tyr Asn Pro Ser Leu Phe Ser Ile Val Thr Asp Asn Gly Ala Gly  
296 290 295 300  
299 Leu Pro Ser Thr Ile Leu Gly Ser Val Ser Tyr Ser Gly Pro Val Pro  
300 305 310 315 320  
303 Pro Arg Ala Leu Pro Ala Ser Cys Lys Ile Ala Cys Lys Pro Val Pro  
304 325 330 335  
307 Thr Ala Pro Gly Thr Asn Pro Thr Glu Tyr Thr Thr Ile Thr Thr  
308 340 345 350  
311 Thr Asn Ser Ala Gly Lys Pro Leu Thr Glu Thr Gly Val Val Asp Ile  
312 355 360 365  
315 Ser Thr Asp Ser Asn Gly Ser Trp Phe Ser Ser Thr Thr Ile Phe Pro  
316 370 375 380  
319 Thr Ser Ser Ser Ser Ser Ser Ser Thr Val Ser Ser Thr Ala  
320 385 390 395 400  
323 Pro Ser Ser Ser Ser Thr Lys Pro Ser Ser Ser Ser Gln Pro Ser Ser  
324 405 410 415  
327 Thr Pro Pro Pro Ser Ser Ser Ser Lys Ala Ser Ser Thr Thr Pro Ser  
328 420 425 430  
331 Ser Ser Ser Gln Ser Ser Ser Thr Thr Pro Ser Ser Ser Ser Lys Pro  
332 435 440 445  
335 Ser Ser Thr Val Pro Pro Thr Gly Ser Ser Gln Ser Ser Ser Thr Ile  
336 450 455 460  
339 Pro Ser Ser Ser Thr Gln Pro Ser Ser Thr Ala Pro Ser Ser Leu Ser  
340 465 470 475 480  
343 Ser Pro Ser Ser Thr Thr Pro Ser Ser Ser Ser Gln Ser Ser Phe  
344 485 490 495  
347 Ser Ala Gln Ser Ser Ile Gly Gln Thr Ser Ser Ser Thr Val Ser Ser  
348 500 505 510  
351 Ser Ser Ser Gln Pro Ser Cys Trp Glu Ser Ser Ser Ser Gln Ser Ser  
352 515 520 525  
355 Ser Gly Thr Thr Ser Ser Ser Ser Gln Phe Ser Ser Ser Ala Pro Pro  
356 530 535 540  
359 Ser Ser Thr Gln Ser Ser Phe Thr Ala Glu Ser Ser Asn Ser Gln Leu

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363	<210> SEQ ID NO: 7			
364	<211> LENGTH: 30			
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373	<211> LENGTH: 29			
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377	<400> SEQUENCE: 8			
378	ccgctcgagt tccaaacttta atcccgac			29
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409	<211> LENGTH: 29			
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417	<210> SEQ ID NO: 13			
418	<211> LENGTH: 36			
419	<212> TYPE: DNA			
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428	<212> TYPE: DNA			
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**VERIFICATION SUMMARY**

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date